

SEQUENCE LISTING

<110> Kindl, Helmut
 May, Christian
 Feussner, Ivo

<120> The N-terminal beta-barrel structure of lipid body lipoxxygenase mediates
 its binding to liposomes and lipid bodies

<130> 99_1235

<140> US 10/089,147

<141> Filing date not yet granted

<150> PCT/EP/00/09912

<151> 2000-10-10

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gga gat ctt gca ggt tct gtt atc aat gct ggt ggt aac att tta gat	96
Gly Asp Leu Ala Gly Ser Val Ile Asn Ala Gly Gly Asn Ile Leu Asp	
20 25 30	
aga gtt tcc agt ctt gga gga aac aaa atc aaa ggg aaa gtg att ctt	144
Arg Val Ser Ser Leu Gly Gly Asn Lys Ile Lys Gly Lys Val Ile Leu	
35 40 45	
atg aga agc aat gtt ttg gat ttc act gaa ttt cat tcc aat ctt ctt	192
Met Arg Ser Asn Val Leu Asp Phe Thr Glu Phe His Ser Asn Leu Leu	
50 55 60	
gat aac ttc act gag ctc ttg ggt ggt ggt gtt tct ttc caa ctc att	240
Asp Asn Phe Thr Glu Leu Leu Gly Gly Gly Val Ser Phe Gln Leu Ile	
65 70 75 80	
agt gcc act cat act tca aat gac tca aga ggg aaa gtt ggg aac aag	288
Ser Ala Thr His Thr Ser Asn Asp Ser Arg Gly Lys Val Gly Asn Lys	
85 90 95	

gca tat ttg gag agg tgg cta act tca atc cca cca ctg ttt gct gga 336
 Ala Tyr Leu Glu Arg Trp Leu Thr Ser Ile Pro Pro Leu Phe Ala Gly
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gaa tca gtg ttc caa atc aac ttt caa tgg gat gaa aat ttt gga ttt 384
 Glu Ser Val Phe Gln Ile Asn Phe Gln Trp Asp Glu Asn Phe Gly Phe
 115 120 125

cca gga gct ttc ttc ata aaa aat gga cat aca agt gaa ttc ttt ctc 432
 Pro Gly Ala Phe Phe Ile Lys Asn Gly His Thr Ser Glu Phe Phe Leu
 130 135 140

aaa tct ctc act ctt gat gat gtt cct ggc tat ggc aga gtc cat ttt 480
 Lys Ser Leu Thr Leu Asp Asp Val Pro Gly Tyr Gly Arg Val His Phe
 145 150 155 160

gat tgc aat tct tgg gtt tac cct tct gga aga tac aag aaa gat cgc 528
 Asp Cys Asn Ser Trp Val Tyr Pro Ser Gly Arg Tyr Lys Lys Asp Arg
 165 170 175

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 Ile Phe Phe Ala Asn His Val Tyr Leu Pro Ser Gln Thr Pro Asn Pro
 180 185 190

ctt cgt aag tat aga gag gaa gaa ttg tgg aat ttg aga gga gat gga 624
 Leu Arg Lys Tyr Arg Glu Glu Glu Leu Trp Asn Leu Arg Gly Asp Gly
 195 200 205

aca gga gaa aga aag gaa tgg gat aga att tat gac tat gat gtt tat 672
 Thr Gly Glu Arg Lys Glu Trp Asp Arg Ile Tyr Asp Tyr Asp Val Tyr
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Met Arg Ser Asn Val Leu Asp Phe Thr Glu Phe His Ser Asn Leu Leu
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 Asp Asn Phe Thr Glu Leu Leu Gly Gly Gly Val Ser Phe Gln Leu Ile
 65 70 75 80
 Ser Ala Thr His Thr Ser Asn Asp Ser Arg Gly Lys Val Gly Asn Lys
 85 90 95
 Ala Tyr Leu Glu Arg Trp Leu Thr Ser Ile Pro Pro Leu Phe Ala Gly
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 Glu Ser Val Phe Gln Ile Asn Phe Gln Trp Asp Glu Asn Phe Gly Phe
 115 120 125
 Pro Gly Ala Phe Phe Ile Lys Asn Gly His Thr Ser Glu Phe Phe Leu
 130 135 140
 Lys Ser Leu Thr Leu Asp Asp Val Pro Gly Tyr Gly Arg Val His Phe
 145 150 155 160
 Asp Cys Asn Ser Trp Val Tyr Pro Ser Gly Arg Tyr Lys Lys Asp Arg
 165 170 175
 Ile Phe Phe Ala Asn His Val Tyr Leu Pro Ser Gln Thr Pro Asn Pro
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 Leu Arg Lys Tyr Arg Glu Glu Glu Leu Trp Asn Leu Arg Gly Asp Gly
 195 200 205
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agt ctt gga gga aac aaa atc aaa ggg aaa gtg att ctt atg aga agc	200
Ser Leu Gly Gly Asn Lys Ile Lys Gly Lys Val Ile Leu Met Arg Ser	
40 45 50	
aat gtt ttg gat ttc act gaa ttt cat tcc aat ctt ctt gat aac ttc	248
Asn Val Leu Asp Phe Thr Glu Phe His Ser Asn Leu Leu Asp Asn Phe	
55 60 65	
act gag ctc ttg ggt ggt ggt gtt tct ttc caa ctc att agt gcc act	296
Thr Glu Leu Leu Gly Gly Gly Val Ser Phe Gln Leu Ile Ser Ala Thr	
70 75 80	
cat act tca aat gac tca aga ggg aaa gtt ggg aac aag gca tat ttg	344
His Thr Ser Asn Asp Ser Arg Gly Lys Val Gly Asn Lys Ala Tyr Leu	
85 90 95	
gag agg tgg cta act tca atc cca cca ctg ttt gct gga gaa tca gtg	392
Glu Arg Trp Leu Thr Ser Ile Pro Pro Leu Phe Ala Gly Glu Ser Val	
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Phe Phe Ile Lys Asn Gly His Thr Ser Glu Phe Phe Leu Lys Ser Leu	
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Thr Leu Asp Asp Val Pro Gly Tyr Gly Arg Val His Phe Asp Cys Asn	
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Ser Trp Val Tyr Pro Ser Gly Arg Tyr Lys Lys Asp Arg Ile Phe Phe	
165 170 175	
gcc aat cat gtt tat ctt cca agt caa aca cca aac cct ctt cgt aag	632
Ala Asn His Val Tyr Leu Pro Ser Gln Thr Pro Asn Pro Leu Arg Lys	
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tat aga gag gaa gaa ttg tgg aat ttg aga gga gat gga aca gga gaa	680
Tyr Arg Glu Glu Glu Leu Trp Asn Leu Arg Gly Asp Gly Thr Gly Glu	
200 205 210	
aga aag gaa tgg gat aga att tat gac tat gat gtt tat aat gac att	728
Arg Lys Glu Trp Asp Arg Ile Tyr Asp Tyr Asp Val Tyr Asn Asp Ile	
215 220 225	
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230 235 240	

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245 250 255	
aga gac cac aat tat gag agc aga ttg tca cca ata atg agc tta gac	872
Arg Asp His Asn Tyr Glu Ser Arg Leu Ser Pro Ile Met Ser Leu Asp	
260 265 270 275	
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Ile Tyr Val Pro Lys Asp Glu Asn Phe Gly His Leu Lys Met Ser Asp	
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ttc ctt ggt tat aca tta aaa gca ctt tgc ata tca atc aaa cca gga	968
Phe Leu Gly Tyr Thr Leu Lys Ala Leu Ser Ile Ser Ile Lys Pro Gly	
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Glu Val Asp Asn Leu Phe Glu Arg Gly Phe Pro Ile Pro Phe Asn Ala	
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Phe Lys Thr Leu Thr Glu Asp Leu Thr Pro Pro Leu Phe Lys Ala Leu	
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Val Arg Asn Asp Gly Glu Lys Phe Leu Lys Phe Pro Thr Pro Glu Val	
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Val Lys Asp Asn Lys Ile Gly Trp Ser Thr Asp Glu Glu Phe Ala Arg	
375 380 385	
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Phe Pro Pro Thr Ser Lys Leu Asp Pro Asn Val Tyr Gly Asn Gln Asn	
405 410 415	
agt acc atc act gaa gaa cac ata aag cat ggt tta gat ggt ctt acg	1352
Ser Thr Ile Thr Glu Glu His Ile Lys His Gly Leu Asp Gly Leu Thr	
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Val Asp Glu Ala Met Lys Gln Asn Arg Leu Tyr Ile Val Asp Phe His	
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Asp Ala Leu Met Pro Tyr Leu Thr Arg Met Asn Ala Thr Ser Thr Lys	
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aca tat gcc aca aga aca ttg ctt ctt ttg aaa gat gat ggg act ttg	1496
Thr Tyr Ala Thr Arg Thr Leu Leu Leu Leu Lys Asp Asp Gly Thr Leu	
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aag cca ttg gtt att gag tta gcc ttg cca cat cct caa gga gat caa	1544
Lys Pro Leu Val Ile Glu Leu Ala Leu Pro His Pro Gln Gly Asp Gln	
485 490 495	
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Leu Gly Ala Ile Ser Lys Leu Tyr Phe Pro Ala Glu Asn Gly Val Gln	
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Lys Ser Ile Trp Gln Leu Ala Lys Ala Tyr Val Thr Val Asn Asp Val	
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Gly Tyr His Gln Leu Ile Ser His Trp Leu His Thr His Ala Val Leu	
535 540 545	
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Ile His Lys Leu Leu Val Pro His Tyr Lys Asp Thr Met Phe Ile Asn	
565 570 575	
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Ala Ser Ala Arg Gln Val Leu Ile Asn Ala Asn Gly Leu Ile Glu Thr	
580 585 590 595	
acc cat tat cca tca aaa tat tca atg gag ttg tca tct atc ttg tac	1880
Thr His Tyr Pro Ser Lys Tyr Ser Met Glu Leu Ser Ser Ile Leu Tyr	
600 605 610	
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Lys Asp Trp Thr Phe Pro Asp Gln Ala Leu Pro Asn Asn Leu Met Lys	
615 620 625	
aga gga cta gct gtg gag gac tca agt gcc ccc cat gga ctt aga ttg	1976
Arg Gly Leu Ala Val Glu Asp Ser Ser Ala Pro His Gly Leu Arg Leu	
630 635 640	
cta ata aat gat tat cca ttt gct gtt gat ggt ctt gac att tgg tca	2024
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645 650 655	
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Ala Ile Lys Thr Trp Val Gln Asp Tyr Cys Cys Leu Tyr Tyr Lys Asp	
660 665 670 675	
gac aat gca gta caa aat gac ttt gaa ctc caa tct tgg tgg aat gag	2120
Asp Asn Ala Val Gln Asn Asp Phe Glu Leu Gln Ser Trp Trp Asn Glu	
680 685 690	

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Leu Arg Glu Lys Gly His Ala Asp Lys Lys His Glu Pro Trp Trp Pro	
695 700 705	
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Lys Met Gln Thr Leu Ser Glu Leu Ile Glu Ser Cys Thr Thr Ile Ile	
710 715 720	
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Trp Ile Ala Ser Ala Leu His Ala Ala Val Asn Phe Gly Gln Tyr Pro	
725 730 735	
tac gga ggc tat att ctc aat cga cca act aca agt cgt agg ttc atg	2312
Tyr Gly Gly Tyr Ile Leu Asn Arg Pro Thr Thr Ser Arg Arg Phe Met	
740 745 750 755	
cct gaa gtt ggc acg gct gag tac aaa gaa ctg gaa tcg aat ccc gaa	2360
Pro Glu Val Gly Thr Ala Glu Tyr Lys Glu Leu Glu Ser Asn Pro Glu	
760 765 770	
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Lys Ala Phe Leu Arg Thr Ile Cys Ser Glu Leu Gln Ala Leu Val Ser	
775 780 785	
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Ile Ser Ile Ile Glu Ile Leu Ser Lys His Ala Ser Asp Glu Val Tyr	
790 795 800	
ctt gga caa aga gct tca att gat tgg act tca gat aaa att gca ttg	2504
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805 810 815	
gaa gca ttt gag aaa ttt ggg aaa aat tta ttt gaa gtt gag aat agg	2552
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840 845 850	
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Val Asn Leu Pro Tyr Thr Leu Leu Val Pro Ser Ser Asn Glu Gly Leu	
855 860 865	
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Thr Gly Arg Gly Ile Pro Asn Ser Ile Ser Ile	
870 875	
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2964

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<212> PRT

<213> Cucumis sativus

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 35 40 45

Met Arg Ser Asn Val Leu Asp Phe Thr Glu Phe His Ser Asn Leu Leu
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Asp Asn Phe Thr Glu Leu Leu Gly Gly Gly Val Ser Phe Gln Leu Ile
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Ser Ala Thr His Thr Ser Asn Asp Ser Arg Gly Lys Val Gly Asn Lys
 85 90 95

Ala Tyr Leu Glu Arg Trp Leu Thr Ser Ile Pro Pro Leu Phe Ala Gly
 100 105 110

Glu Ser Val Phe Gln Ile Asn Phe Gln Trp Asp Glu Asn Phe Gly Phe
 115 120 125

Pro Gly Ala Phe Phe Ile Lys Asn Gly His Thr Ser Glu Phe Phe Leu
 130 135 140

Lys Ser Leu Thr Leu Asp Asp Val Pro Gly Tyr Gly Arg Val His Phe
 145 150 155 160

Asp Cys Asn Ser Trp Val Tyr Pro Ser Gly Arg Tyr Lys Lys Asp Arg
 165 170 175

Ile Phe Phe Ala Asn His Val Tyr Leu Pro Ser Gln Thr Pro Asn Pro
 180 185 190

Leu Arg Lys Tyr Arg Glu Glu Glu Leu Trp Asn Leu Arg Gly Asp Gly
 195 200 205

Thr Gly Glu Arg Lys Glu Trp Asp Arg Ile Tyr Asp Tyr Asp Val Tyr
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Asn Asp Ile Ala Asp Pro Asp Val Gly Asp His Arg Pro Ile Leu Gly
 225 230 235 240

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Ala Val Leu Glu Pro Phe Val Ile Ala Thr His Arg Gln Leu Ser Val
 545 550 555 560
 Leu His Pro Ile His Lys Leu Leu Val Pro His Tyr Lys Asp Thr Met
 565 570 575
 Phe Ile Asn Ala Ser Ala Arg Gln Val Leu Ile Asn Ala Asn Gly Leu
 580 585 590
 Ile Glu Thr Thr His Tyr Pro Ser Lys Tyr Ser Met Glu Leu Ser Ser
 595 600 605
 Ile Leu Tyr Lys Asp Trp Thr Phe Pro Asp Gln Ala Leu Pro Asn Asn
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 625 630 635 640
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 645 650 655
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 660 665 670
 Tyr Lys Asp Asp Asn Ala Val Gln Asn Asp Phe Glu Leu Gln Ser Trp
 675 680 685
 Trp Asn Glu Leu Arg Glu Lys Gly His Ala Asp Lys Lys His Glu Pro
 690 695 700
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 Arg Phe Met Pro Glu Val Gly Thr Ala Glu Tyr Lys Glu Leu Glu Ser
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 Asn Pro Glu Lys Ala Phe Leu Arg Thr Ile Cys Ser Glu Leu Gln Ala
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Ser Gly Pro Val Asn Leu Pro Tyr Thr Leu Leu Val Pro Ser Ser Asn
850 855 860

Glu Gly Leu Thr Gly Arg Gly Ile Pro Asn Ser Ile Ser Ile
865 870 875